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1  M F K S L T K V N K V K P I G E N N E N E Q S S R R N E E G S H P S N Q S Q Q T T A Q E E N K G E E K S L K T K S T P V Cng3BFL.pro
1  M - - - - - - - - - - A K I N T Q Y S H P S R - - - - - T H L K V K T S D R D L N R A E N G L S R A H S S S E E T S CNGA3.pro
1  M - - - - - K L S - M K N N I I N T Q Q S F V T M - - - - - P N V I V P D I E K E I R R M E N G A C S S F S E D D D S A CNGA1.pro

61  T S E E P H T N I Q D K L S K K N S S G D L T T N P D P Q N A A E P T G T V P E Q K E M D F G K E G P N S P Q N K P P A Cng3BFL.pro
44  S V L Q P G I A M E T R G L A D S G Q G S F T G Q - - - - - G I A R L S - - - R L I F L - - L R R W A A R H V H H Q CNGA3.pro
50  S T S E - - - - - E S E N E N P H A R G S F S Y K - - - - - S L R K G G P S Q R E Q Y L P G A I A L F N V N S S N K CNGA1.pro

121 A P V I N E Y A D A Q L H N L V K R M R Q R T A L Y K K K L V E G D L S S P E A S P Q T A K P T A V P P V K E S D D K P Cng3BFL.pro
92  D Q G P D S F P D R F R G A E L K E V S S Q E S N A Q A N V G S Q E P A D R G R S A W P L A K C N T N T S N N T E E E K CNGA3.pro
99  D Q E P E E - - - - - K K K K K K E K S S D D K N E N K N D P E K K K K K K D K E K K K K E E K S K D K K CNGA1.pro

181 T E H Y Y R L L W F K V K K M P L T E Y L K R I K L P N S I D S Y T D R L Y L L W L L V T L A - - Y N W N C W F I P L Cng3BFL.pro
152 K T K - - - - - - - K K D A I V - - - - - V D P - S S N L Y Y R W L T A I A L P V F Y N W Y - - L L I C CNGA3.pro
149 E E E - - - - - - - K K E V V - - - - - I D P - S G N T Y Y N W L F C I T L P V M Y N W T - - M V I A CNGA1.pro

239 R L V F P Y Q T A D N I H Y W L I A D I I C D I I Y L Y D M L F I Q P R L Q F V R G G D I I V D S N E L R K H Y R T S P Cng3BFL.pro
189 R A C F D E L O S E Y L M L W L V L D Y S A D V L Y V L D V - L V R A R T C F L E O G L M V S D T N R L W Q H Y K T T T CNGA3.pro
186 R A C F D E L Q S D Y L E Y W L I L D Y V S D I V Y L I D M - F V R T R T G Y L E O G L L W K E E L K L I N K Y K S N L CNGA1.pro

299 K F Q L D V A S I I P F D I C Y L F F G F N - P M F R A N R M L K Y T S F F E F N H H L E S I M D K A Y I Y R V I R T T Cng3BFL.pro
248 Q F K L D V L S L V P T D L A Y L K V G T N Y P E V R E N R L L K F S R L P E F F D R T E T R T N Y P N M F R I G N L V CNGA3.pro
245 Q F K L D V L S L I P T D L L Y F K L G W N Y P E I R L N R L L R P S R M F E F F Q R T E T R T N Y P N I F R I S N L V CNGA1.pro

358 G Y L L F I L H I N A C V Y Y W A S N Y E G I G T T R W V Y D G E G N - - - - - E Y L R C Y Y W A V R T L I T I G Cng3BFL.pro
308 Y I L I I I H W N A C I Y F A I S K F I G F G T D S W V Y P N I S I P E H G R L S R K Y I Y S L Y W S T L T L T T I G CNGA3.pro
305 Y I V I I I H W N A C V F Y S I S K A I G F G N D T W V Y P D I N D P E F G R L A R K Y V Y S L Y W S T L T L T T I G CNGA1.pro

410 G L P E P Q T L F E I V F Q L L N F F S G V F V F S S L I G Q M R D V I G A A T A N Q N Y F R A C M D D T I A Y M N N Y Cng3BFL.pro
368 E T P P P V K D E E Y L E V V V D F L V G V L I F A T I V G N V G S M I S N M N A S R A E F O A K I D S I K Q Y M Q F R CNGA3.pro
365 E T P P P V R D S E Y V F V V V D F L I G V L I F A T I V G N I G S M I S N M N A A R A E F O A R I D A I K Q Y M H F R CNGA1.pro

470 S I P K L V Q K R V R T W Y E Y T W D S Q R M L D E S D L L K T L P T T V Q L A L A I D V N F S I I S K V D L F K G C D Cng3BFL.pro
428 V T K D L E T R V I R W F D Y L W A N K K T V D E K E V L K S L P D K L K A E I A I N V H L D T L K K V R I E Q D C E CNGA3.pro
425 V S K D M E K R V I K W F D Y L W T N K K T V D E K E V L K Y L P D K L R A E I A I N V H L D T L K K V R I E A D C E CNGA1.pro

530 T Q M I Y D M L L R L K S V L Y L P G D F V C K K G E I G K E M Y I I K H G E V Q V L G G P D G T K V L V T L K A G S V Cng3BFL.pro
488 A G L L V E L V L K L R P T V F S P G D Y I C K K G D I G K E M Y I I N E G K L A V V A D - D G V T Q F V V L S D G S Y CNGA3.pro
485 A G L L V E L V L K L Q P Q V Y S P G D Y I C K K G D I G R E M Y I I K E G K L A V V A D - D G V T Q F V V L S D G S Y CNGA1.pro

590 F G E I S L L A A G G - - - G N R R T A N V V A H G F A N L L T L D K K T L Q E I L V H Y P D S E R I L M K K A R - V L Cng3BFL.pro
547 F G E I S I L N I K G S K S G N R R T A N I R S I G Y S D L F C L S K D D L M E A L T E Y P E A K K A L E E K G R Q I L CNGA3.pro
544 F G E I S I L N I K G S K A G N R R T A N I K S I G Y S D L F C L S K D D L M E A L T E Y P D A K T M L E E K G K Q I L CNGA1.pro

646 L K Q K A K T A E A T P P R K D L A L L F P P K E E T P K L F K T L L G G T G K A S L A R L L K L K R E Q A A Q K K E N Cng3BFL.pro
607 M K D N L I D E E L A R A G A D - - - - - P K D L E E K V - - E Q L G S S L D T L Q T R F A R L L - - - - - CNGA3.pro
604 M K D G L L D L N I A N A G S D - - - - - P K D L E E K V - - T R M E G S V D L L Q T R F A R I L - - - - - CNGA1.pro

706 S B G G E E E G K E N E D K Q K E N E D K Q K E N E D K G K E N R D K D K G R E P E E K P L D R P E C T A S P I A V E E Cng3BFL.pro
649 - - - - - - - A E Y N A T Q M K M K Q R L S Q L E S Q V K G G D K - - - - - - - - - - - P L A D G B CNGA3.pro
646 - - - - - - - A E Y E S M Q Q K L K Q R L T K V E K F L K P L I D T - - - - - - - - - - - E F S S I E CNGA1.pro

766 E P H S V R R T V L P R G T S R Q S L I I S M A P S A E G G E E V L T I E V K E K A K Q . Cng3BFL.pro
682 V P - - - - - - - - - - - - - - - - - - - - - G D A T K T E D - - - - - K Q Q . CNGA3.pro
679 G P - - - - - - - - - - - - - - - - - - - - - G A E S G P I D - - - - - S T . CNGA1.pro

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Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.?

Figure 1

CNG3B DNA SEQUENCE

CCATCCTAATACGACTCACTATAGGGCTCGAGCGGCCGCCGGGCAGGTCATTTCTCTACCTTAAGGCACAGTCATA
AATACAGAGGGTTTTTCAGAACACCTCAGAGAAGATGTTTAAATCGCTGACAAAAGTCAACAAGGTGAAGCCTATAG
GAGAGAACAATGAGAATGAACAAAGTTCTCGTCGGAATGAAGAAGGCTCTACCCAAGTAATCAGTCTCAGCAAACC
ACAGCACAGGAAGAAAACAAAGGTGAAGAGAAATCTCTCAAACCAAGTCAACTCCAGTCACGTCTGAAGAGCCACA
CACCAACATACAAGACAACTCTCCAAGAAAAATTCCTCTGGAGATCTGACCACAAACCCTGACCCTCAAAATGCAG
CAGAACCAACTGGAACAGTGCCAGAGCAGAAGGAAATGGACCCCGGGAAGAAGGTCCAAACAGCCCACAAAACAAA
CCGCCTGCAGCTCCTGTTATAAATGAGTATGCCGATGCCAGCTACACAACCTGGTGAAAAAGAATGCGTCAAAGAAC
AGCCCTCTACAAGAAAAAGTTGGTAGAGGGAGATCTCTCCTCACCCGAAGCCAGCCCACAACTGCAAAGCCCACGG
CTGTACCACCAGTAAAAGAAAGCGATGATAAGCCAACAGAACATTACTACAGGCTGTTGTGGTTCAAAGTCAAAAAG
ATGCCTTTAACAGAGTACTTAAAGCGAATTAACTTCCAAACAGCATAGATTTCATACACAGATCGACTCTATCTCCT
GTGGCTCTTGCTTGTCACTCTTGCTTATAACTGGAAGTCTGGTTTATACCACTGCGCCTCGTCTTCCCATATCAAA
CCGCAGACAACATACTACTGGCTTATTGCGGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATC
CAGCCCAGACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGGATTCAAATGAGCTAAGGAAACACTACAGGACTTC
TACAAAATTTTCAAGTGTGCGATCAATAATACCATTGATATTTGCTACCTCTTCTTTGGGTTTAAATCCAATGT
TTAGAGCAAATAGGATGTTAAAGTACACTTCATTTTTTGAATTTAATCATCACCTAGAGTCTATAATGGACAAAGCA
TATATCTACAGAGTTATTTCGAACAACCTGGATACTTGCTGTTTATTTCTGCACATTAATGCCTGTGTTTATTACTGGGC
TTCAAACCTATGAAGGAATTGGCACTACTAGATGGGTGTATGATGGGGAAGGAAACGAGTATCTGAGATGTTATTATT
GGGCAGTTCGAACTTTAATTACCATTGGTGGCCTTCCAGAACCACAACTTTATTTGAAATTGTTTTTCAACTCTTG
AATTTTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAATTGGTCAGATGAGAGATGTGATTGGAGCAGCTACAGCCAA
TCAGAACTACTTCCGCGCCTGCATGGATGACACCATTGCCTACATGAACAATTACTCCATTCCCTAACTTGTGCAAA
AGCGAGTTCGGAATTGGTATGAATATACATGGGACTCTCAAAGAATGCTAGATGAGTCTGATTTGCTTAAGACCCTA
CCAACCTACGGTCCAGTTAGCCCTCGCCATTGATGTGAACCTCAGCATCATCAGCAAAGTCGACTTGTTCAGGGTTG
TGATACACAGATGATTTATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTTGCCTGGTGACTTTGTCTGCAAAA
AGGGAGAAATTGGCAAGGAAATGTATATCATCAAGCATGGAGAAGTCCAAGTTCTTGGAGGCCCTGATGGTACTAAA
GTTCTGGTTACTCTGAAAGCTGGGTCCGTTGTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGGAAACCGTCGAAC
TGCCAAATGTGGTGGCCACGGGTTTGCCAATCTTTTAACTCTAGACAAAAGACCCTCCAAGAAATTCTAGTGCATT
ATCCAGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGCTTTTAAAGCAGAAGGCTAAGACCGCAGAAGCAACC
CTCCAAGAAAAGATCTTGCCCTCCTCTTCCCACCGAAAGAAGAGACACCCAACTGTTTAAACTCTCCTAGGAGG
CACAGGAAAAGCAAGTCTTGCAAGACTACTCAAATTGAAGCGAGAGCAAGCAGCTCAGAAGAAAGAAAATTCTGAAG
GAGGAGAGGAAGAAGGAAAAGAAAATGAAGATAAAACAAAAGAAAATGAAGATAAAACAAAAGAAAATGAAGATAAA
GGAAAAGAAAATGAAGATAAAAGATAAAAGGAAGAGAGCCAGAAGAGAAGCCACTGGACAGACCTGAATGTACAGCAAG
TCCTATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGACAGTTTTACCCAGAGGGACTTCTCGTCAATCACTCA
TTATCAGCATGGCTCCTTCTGCTGAGGGCGGAGAAGAGGTTCTTACTATTGAAGTCAAAGAAAAGGCTAAGCAATAA
ATGTTTGATTATCTTTAGATGTGATATAGCTAGTTCCCAAAGTGATTGTACCTAGGATTGTAACCTAAATTAACGAG
GGGAAACGACATGCTGGGACCCTTGAGAAACGAAAGGCAAATCCCTAGCTTAGTTTCTAGGACTTATCTGAGAGTGT
GATTTTCATGCAGTGGTAATAAGAAGATTATTTAAAGCAAAAAAAAAAAAAAAAAAAAAAAAAA

Figure 2

CNG3B Coding Sequence

ATGTTTAAATCGCTGACAAAAGTCAACAAGGTGAAGCCTATAGGAGAGAACAATGAGAATGAACAAAGTTCTCGTCGGAA
TGAAGAAGGCTCTCACCCAAGTAATCAGTCTCAGCAAACCACAGCACAGGAAGAAAACAAAGGTGAAGAGAAATCTCTCA
AAACCAAGTCAACTCCAGTCACGTCTGAAGAGCCACACACCAACATACAAGACAAACTCTCCAAGAAAAATTCCTCTGGA
GATCTGACCACAAACCCTGACCCTCAAAATGCAGCAGAACCAACTGGAACAGTGCCAGAGCAGAAGGAAATGGACCCCCGG
GAAAGAAGGTCCAAACAGCCCACAAAACAAACCGCCTGCAGCTCCTGTTATAAATGAGTATGCCGATGCCAGCTACACA
ACCTGGTGAAGAAGTTCGTCAAAGAACAGCCCTCTACAAGAAAAAGTTGGTAGAGGGAGATCTCTCCTCACCCGAAGCC
AGCCCACAAACTGCAAAGCCCACGGCTGTACCACAGTAAAAGAAAGCGATGATAAGCCAACAGAACATTACTACAGGCT
GTTGTGGTTCAAAGTCAAAAAGATGCCTTTAACAGAGTACTTAAAGCGAATTAAACTTCCAAACAGCATAGATTATACA
CAGATCGACTCTATCTCCTGTGGCTCTTGCTTGTCACTCTTGCTTATAACTGGAACGCTGGTTTATACCACTGCGCCTC
GTCTTCCCATATCAAACCGCAGACAACATACACTACTGGCTTATTGCGGACATCATATGTGATATCATCTACCTTTATGA
TATGCTATTTATCCAGCCCAGACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGGATTCAAATGAGCTAAGGAAACACT
ACAGGACTTCTACAAAATTTTCAGTTGGATGTGCGCATCAATAATACCATTTGATATTTGCTACCTCTTCTTTGGGTTTAAT
CCAATGTTTAGAGCAAATAGGATGTTAAAGTACACTTCATTTTTTTGAATTTAATCATCACCTAGAGTCTATAATGGACAA
AGCATATATCTACAGAGTTATTGGAACAACCTGGATACTTGCTGTTTATTCTGCACATTAATGCCTGTGTTTATTACTGGG
CTTCAAACATATGAAGGAATTGGCACTACTAGATGGGTGTATGATGGGGAAGGAAACGAGTATCTGAGATGTTATTATTGG
GCAGTTGCAACTTTAATTACCATTGGTGGCCTTCCAGAACCACAACTTTATTTGAAATTGTTTTTCAACTCTTGAATTT
TTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAATTGGTCAGATGAGAGATGTGATTGGAGCAGCTACAGCCAATCAGAACT
ACTTCCGCGCCTGCATGGATGACACCATTGCCTACATGAACAATTACTCCATTCTAAACTTGTGCAAAGCGAGTTCGG
ACTTGGTATGAATATACATGGGACTCTCAAAGAATGCTAGATGAGTCTGATTTGCTTAAGACCCTACCAACTACGGTCCA
GTTAGCCCTCGCCATTGATGTGAACCTCAGCATCATCAGCAAAGTCGACTTGTTCAAGGGTTGTGATACACAGATGATTT
ATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTTGCCTGGTGAAGTTTGTCTGCAAAAAGGGAGAAATTTGGCAAGGAA
ATGTATATCATCAAGCATGGAGAAGTCCAAGTTCTTGGAGGCCCTGATGGTACTAAAGTTCTGGTTACTCTGAAAGCTGG
GTCGGTGTGTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAGGAAACCGTCAACTGCCAATGTGGTGGCCACGGGTTTG
CCAATCTTTTAACTCTAGACAAAAGACCCTCCAAGAAATTTAGTGCATTATCCAGATTCTGAAAGGATCCTCATGAAG
AAAGCCAGAGTGCTTTTAAAGCAGAAGGCTAAGACCGCAGAAGCAACCCCTCCAAGAAAAGATCTTGCCCTCCTCTTCCC
ACCGAAAGAAGAGACACCCAACTGTTTAAACTCTCCTAGGAGGCACAGGAAAAGCAAGTCTTGCAAGACTACTCAAT
TGAAGCGAGAGCAAGCAGCTCAGAAGAAAGAAAATTTCTGAAGGAGGAGAGGAAGAAGGAAAAGAAAATGAAGATAAACAA
AAAGAAAATGAAGATAAACAAAAGAAAATGAAGATAAAGGAAAAGAAAATGAAGATAAAGATAAAGGAAGAGAGCCAGA
AGAGAAGCCACTGGACAGACCTGAATGTACAGCAAGTCCTATTGCAGTGGAGGAAGAACCCCACTCAGTTAGAAGGACAG
TTTTACCCAGAGGACTTCTCGTCAATCACTCATTATCAGCATGGCTCCTTCTGCTGAGGGCGGAGAAGAGGTTCTTACT
ATTGAAGTCAAAGAAAAGGCTAAGCAATAA

Figure 3

CNG3B amino acid sequence

MFKSLTKVNKVKPIGENNENEQSSRRNEEGSHPSNQSQQTAEENKGEEKSLKTKSTPVTS
EEPHTNIQDKLSKKNSSGDLTTNPDQNAAEPTGTVPQKEMDPGKEGPNSPQNKPPAAPVI
NEYADAQLHNLVKRMRQRTALYKKKLVEGDLSSPEASPQTAKPTAVPPVKESDDKPTEHYR
LLWFKVKKMPLTEYLKRIKLPNSIDSYTDRLYLLWLLLVTLAYNWNCFIPLRLVFPYQTAD
NIHYWLIADIICDIIYLYDMLFIQPRLOFVRGGDIIIVDSNELRKHYRTSTKFQLDVASII PF
DICYLFFGFNPMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYLLFILHINACVYY
WASNYEGIGTTRWVYDGEENEYLRCCYWAVRTLITIGGLPEPQTLFEIVFQLLNFFSGVFVF
SSLIGQMRDVIGAATANQNYFRACMODTIAYMNNYSIPKLVQKRVRTWYEYTWDSQRMLDES
DLLKTLPTTVQLALADVNFSIIISKVDLFGKCDTQMIYDMLRLKSVLYLPGDFVCKKGEIG
KEMYIIKHGEVQVLGGPDGKVLVTLKAGSVFGEISLLAAGGGNRRTANVVAHGAFANLLTLD
KKTLLQEILVHYPDSERILMKKARVLLKQAKTAEATPPRKDLALLFPPKEETPKLFKTLGG
TGKASLARLLKLKREQAAQKKENSEGEGEEGKENEKQKENEKQKENEKQKENEKQKENEKQKGR
EPEEKPLDRPECTASPIAVEEEPHSVRRTVLPRGTSRQSLIISMAPSAEGGEEVLTIEVKEK
AKQ

Figure 4